



IFWO

RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/10/764,604

TIME: 11:08:06

Input Set : A:\sequence.listing.ascii.txt

Output Set: N:\CRF4\08272004\J764604.raw

3 <110> APPLICANT: McLachlan, Karen
 4 Glaser, Scott
 5 Peach, Robert
 6 Rowe, Anthony
 8 <120> TITLE OF INVENTION: Compositions and Methods for Treating Cancer Using IGSF9 and
 9 LIV-1
 11 <130> FILE REFERENCE: 2159.0030001
 13 <140> CURRENT APPLICATION NUMBER: US 10/764,604
 14 <141> CURRENT FILING DATE: 2004-01-27
 16 <150> PRIOR APPLICATION NUMBER: US 60/442,535
 17 <151> PRIOR FILING DATE: 2003-01-27
 19 <160> NUMBER OF SEQ ID NOS: 43
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 3490
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
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 33 tgtgacctgc tgccccggc cgcccgccc cccctgcatg tcctcgagt gctgcgcttt 180
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 41 gattttgcta acggctcctg ggtgcatctg acagtcaatt caccctctca attccaggag 420
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 47 cagggccagg tgcaagtga gaacgggacg ctgcggatcc gccgggtaga gcgaggcagc 600
 49 tctggggtct acacctgcca agcctccagc actgagggca gcgccacca cgccaccag 660
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79  tggttttgcc caaggggtgcc aatgtctcct gggagcctgg ctttgatggg gggttatctgc 1560
81  agagattcag tgtctggtac accccactgg ccaagcgtcc tgaccgaatg caccatgact 1620
83  ggggtgtcctt ggcagtgcct gtgggggctg ctacacctct agtgccaggg ctgcagcccc 1680
85  acacccagta ccagttcagc gtgctagctc agaacaagct ggggagtggg cctttcagcg 1740
87  aaatcgctctt gtctgctccg gaagggttc ctaccacgcc agctgcaccc gggcttcccc 1800
89  caacagagat accgcctccc ctgtccctc cgcggggtct ggtggcagtg aggacacccc 1860
91  ggggggtact cctgcattgg gatcccccag agctggctcc taagagactg gatggctacg 1920
93  tcttggaagg cgggaaggc tcccagggtt gggagtgctt ggacccggct gtggcaggca 1980
95  cagaaacaga gctgctgggt ccaggcctca tcaaggatgt tctctacgag ttccgcctcg 2040
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125 ccagggaatc acttctctgg gctgtggtag gggctggggc cactgcagag ccccttaca 2940
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133 ctgggcccagt ggccctgaga gatggccccg aaggggagcat gtggtgacag tcagcaagag 3180
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141 ccctgaggcc cgctgtgctg cccttcggga ggaattcctg gccttcgcc gccgccgaga 3420
143 tgctactagg gctcggctac cagcctatcg acagccagtc cccacccccg aacaggccac 3480
145 tctgctgtga                                     3490

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148 <210> SEQ ID NO: 2

149 <211> LENGTH: 1163

150 <212> TYPE: PRT

151 <213> ORGANISM: Homo sapiens

153 <400> SEQUENCE: 2

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155 Met Val Trp Cys Leu Gly Leu Ala Val Leu Ser Leu Val Ile Ser Gln
156 1          5          10          15
159 Gly Ala Asp Gly Arg Gly Lys Pro Glu Val Val Ser Val Val Gly Arg
160          20          25          30
163 Ala Glu Glu Ser Val Val Leu Gly Cys Asp Leu Leu Pro Pro Ala Gly
164          35          40          45
167 Arg Pro Pro Leu His Val Ile Glu Trp Leu Arg Phe Gly Phe Leu Leu
168          50          55          60
171 Pro Ile Phe Ile Gln Phe Gly Leu Tyr Ser Pro Arg Ile Asp Pro Asp
172 65          70          75          80

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175 Tyr Val Gly Arg Val Arg Leu Gln Lys Gly Ala Ser Leu Gln Ile Glu
176                               85                      90                      95
179 Gly Leu Arg Val Glu Asp Gln Gly Trp Tyr Glu Cys Arg Val Phe Phe
180                               100                     105                     110
183 Leu Asp Gln His Ile Pro Glu Asp Phe Ala Asn Gly Ser Trp Val
184                               115                     120                     125
187 His Leu Thr Val Asn Ser Pro Gln Phe Gln Glu Thr Pro Pro Ala
188                               130                     135                     140
191 Val Leu Glu Val Gln Glu Leu Glu Pro Val Thr Leu Arg Cys Val Ala
192 145                               150                     155                     160
195 Arg Gly Ser Pro Leu Pro His Val Thr Trp Lys Leu Arg Gly Lys Asp
196                               165                     170                     175
199 Leu Gly Gln Gly Gln Gly Gln Val Gln Val Gln Asn Gly Thr Leu Arg
200                               180                     185                     190
203 Ile Arg Arg Val Glu Arg Gly Ser Ser Gly Val Tyr Thr Cys Gln Ala
204                               195                     200                     205
207 Ser Ser Thr Glu Gly Ser Ala Thr His Ala Thr Gln Leu Leu Val Leu
208                               210                     215                     220
211 Gly Pro Pro Val Ile Val Val Pro Pro Lys Asn Ser Thr Val Asn Ala
212 225                               230                     235                     240
215 Ser Gln Asp Val Ser Leu Ala Cys His Ala Glu Ala Tyr Pro Ala Asn
216                               245                     250                     255
219 Leu Thr Tyr Ser Trp Phe Gln Asp Asn Ile Asn Val Phe His Ile Ser
220                               260                     265                     270
223 Arg Leu Gln Pro Arg Val Gln Ile Leu Val Asp Gly Ser Leu Arg Leu
224                               275                     280                     285
227 Leu Ala Thr Gln Pro Asp Asp Ala Gly Cys Tyr Thr Cys Val Pro Ser
228                               290                     295                     300
231 Asn Gly Leu Leu His Pro Pro Ser Ala Ser Ala Tyr Leu Thr Val Leu
232 305                               310                     315                     320
235 Cys Met Pro Gly Val Ile Arg Cys Pro Val Arg Ala Asn Pro Pro Leu
236                               325                     330                     335
239 Leu Phe Val Ser Trp Thr Lys Asp Gly Lys Ala Leu Gln Leu Asp Lys
240                               340                     345                     350
243 Phe Pro Gly Trp Ser Gln Gly Thr Glu Gly Ser Leu Ile Ile Ala Leu
244                               355                     360                     365
247 Gly Asn Glu Asp Ala Leu Gly Glu Tyr Ser Cys Thr Pro Tyr Asn Ser
248                               370                     375                     380
251 Leu Gly Thr Ala Gly Pro Ser Pro Val Thr Arg Val Leu Leu Lys Ala
252 385                               390                     395                     400
255 Pro Pro Ala Phe Ile Glu Arg Pro Lys Glu Glu Tyr Phe Gln Glu Val
256                               405                     410                     415
259 Gly Arg Glu Leu Leu Ile Pro Cys Ser Ala Gln Gly Asp Pro Pro Pro
260                               420                     425                     430
263 Val Val Ser Trp Thr Lys Val Gly Arg Gly Leu Gln Gly Gln Ala Gln
264                               435                     440                     445
267 Val Asp Ser Asn Ser Ser Leu Ile Leu Arg Pro Leu Thr Lys Glu Ala
268                               450                     455                     460
271 His Gly His Trp Glu Cys Ser Ala Ser Asn Ala Val Ala Arg Val Ala

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272 465          470          475          480
275 Thr Ser Thr Asn Val Tyr Val Leu Gly Thr Ser Pro His Val Val Thr
276          485          490          495
279 Asn Val Ser Val Val Ala Leu Pro Lys Gly Ala Asn Val Ser Trp Glu
280          500          505          510
283 Pro Gly Phe Asp Gly Gly Tyr Leu Gln Arg Phe Ser Val Trp Tyr Thr
284          515          520          525
287 Pro Leu Ala Lys Arg Pro Asp Arg Met His His Asp Trp Val Ser Leu
288          530          535          540
291 Ala Val Pro Val Gly Ala Ala His Leu Leu Val Pro Gly Leu Gln Pro
292 545          550          555          560
295 His Thr Gln Tyr Gln Phe Ser Val Leu Ala Gln Asn Lys Leu Gly Ser
296          565          570          575
299 Gly Pro Phe Ser Glu Ile Val Leu Ser Ala Pro Glu Gly Leu Pro Thr
300          580          585          590
303 Thr Pro Ala Ala Pro Gly Leu Pro Pro Thr Glu Ile Pro Pro Pro Leu
304          595          600          605
307 Ser Pro Pro Arg Gly Leu Val Ala Val Arg Thr Pro Arg Gly Val Leu
308          610          615          620
311 Leu His Trp Asp Pro Pro Glu Leu Val Pro Lys Arg Leu Asp Gly Tyr
312 625          630          635          640
315 Val Leu Glu Gly Arg Gln Gly Ser Gln Gly Trp Glu Val Leu Asp Pro
316          645          650          655
319 Ala Val Ala Gly Thr Glu Thr Glu Leu Leu Val Pro Gly Leu Ile Lys
320          660          665          670
323 Asp Val Leu Tyr Glu Phe Arg Leu Val Ala Phe Ala Gly Ser Phe Val
324          675          680          685
327 Ser Asp Pro Ser Asn Thr Ala Asn Val Ser Thr Ser Gly Leu Glu Val
328          690          695          700
331 Tyr Pro Ser Arg Thr Gln Leu Pro Gly Leu Leu Pro Gln Pro Val Leu
332 705          710          715          720
335 Ala Gly Val Val Gly Gly Val Cys Phe Leu Gly Val Ala Val Leu Val
336          725          730          735
339 Ser Ile Leu Ala Gly Cys Leu Leu Asn Arg Arg Arg Ala Ala Arg Arg
340          740          745          750
343 Arg Arg Lys Arg Leu Arg Gln Asp Pro Pro Leu Ile Phe Ser Pro Thr
344          755          760          765
347 Gly Lys Ser Ala Ala Pro Ser Ala Leu Gly Ser Gly Ser Pro Asp Ser
348          770          775          780
351 Val Ala Lys Leu Lys Leu Gln Gly Ser Pro Val Pro Ser Leu Arg Gln
352 785          790          795          800
355 Ser Leu Leu Trp Gly Asp Pro Ala Gly Thr Pro Ser Pro His Pro Asp
356          805          810          815
359 Pro Pro Ser Ser Arg Gly Pro Leu Pro Leu Glu Pro Ile Cys Arg Gly
360          820          825          830
363 Pro Asp Gly Arg Phe Val Met Gly Pro Thr Val Ala Ala Pro Gln Glu
364          835          840          845
367 Arg Ser Gly Arg Glu Gln Ala Glu Pro Arg Thr Pro Ala Gln Arg Leu
368          850          855          860

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371 Ala Arg Ser Phe Asp Cys Ser Ser Ser Ser Pro Ser Gly Ala Pro Gln
372 865      870      875      880
375 Pro Leu Cys Ile Glu Asp Ile Ser Pro Val Ala Pro Pro Ala Ala
376      885      890      895
379 Pro Pro Ser Pro Leu Pro Gly Pro Gly Pro Leu Leu Gln Tyr Leu Ser
380      900      905      910
383 Leu Pro Phe Arg Glu Met Asn Val Asp Gly Asp Trp Pro Pro Leu
384      915      920      925
387 Glu Glu Pro Ser Pro Ala Ala Pro Pro Asp Tyr Met Asp Thr Arg Arg
388      930      935      940
391 Cys Pro Thr Ser Ser Phe Leu Arg Ser Pro Glu Thr Pro Pro Val Ser
392 945      950      955      960
395 Pro Arg Glu Ser Leu Pro Gly Ala Val Val Gly Ala Gly Ala Thr Ala
396      965      970      975
399 Glu Pro Pro Tyr Thr Ala Leu Ala Asp Trp Thr Leu Arg Glu Arg Leu
400      980      985      990
403 Leu Pro Gly Leu Leu Pro Ala Ala Pro Arg Gly Ser Leu Thr Ser Gln
404      995      1000      1005
407 Ser Ser Gly Arg Gly Ser Ala Ser Phe Leu Arg Pro Pro Ser Thr
408      1010      1015      1020
411 Ala Pro Ser Ala Gly Gly Ser Tyr Leu Ser Pro Ala Pro Gly Asp
412      1025      1030      1035
415 Thr Ser Ser Trp Ala Ser Gly Pro Glu Arg Trp Pro Arg Arg Glu
416      1040      1045      1050
419 His Val Val Thr Val Ser Lys Arg Arg Asn Thr Ser Val Asp Glu
420      1055      1060      1065
423 Asn Tyr Glu Trp Asp Ser Glu Phe Pro Gly Asp Met Glu Leu Leu
424      1070      1075      1080
427 Glu Thr Leu His Leu Gly Leu Ala Ser Ser Arg Leu Arg Pro Glu
428      1085      1090      1095
431 Ala Glu Thr Glu Leu Gly Val Lys Thr Pro Glu Glu Gly Cys Leu
432      1100      1105      1110
435 Leu Asn Thr Ala His Val Thr Gly Pro Glu Ala Arg Cys Ala Ala
436      1115      1120      1125
439 Leu Arg Glu Glu Phe Leu Ala Phe Arg Arg Arg Arg Asp Ala Thr
440      1130      1135      1140
443 Arg Ala Arg Leu Pro Ala Tyr Arg Gln Pro Val Pro His Pro Glu
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447 Gln Ala Thr Leu Leu
448      1160
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452 <211> LENGTH: 2862
453 <212> TYPE: DNA
454 <213> ORGANISM: Homo sapiens
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461 tgtgacctgc tgcccccggc cgcccgcccc ccctgcatg tcacgagtg gctgcgcttt      180
463 ggattcctgc ttcccatctt catccagttc ggcctctact ctccccgaat tgaccctgat      240

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VERIFICATION SUMMARY

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